

SEQUENCE LISTING

<110> Farnham, Peggy J.
Graveel, Carrie R.
Harkins-Perry, Sarah R.

<120> Liver Tumor marker Sequences

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<223> From this position forward, first variant 3' UTR
sequence reads aaccattaaaaaaaaaaaaaaaaaaagt

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sequence reads
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Val Pro Ile Arg Val Met Ile Asp Leu Cys Asn Ser Thr Gln Gly Ile
10 15 20 25

tgc ctc aca gga cca ccc ggc cca cca gga cct cca gga gcc ggc ggg 147
Cys Leu Thr Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly Ala Gly Gly
30 35 40

tta cca ggc cac aat gga tca gat gga cag cct ggt ctc cag ggc cca 195
Leu Pro Gly His Asn Gly Ser Asp Gly Gln Pro Gly Leu Gln Gly Pro

45	50	55	
aaa gga gaa aaa gga gca att ggc aag aga gga aaa atg ggg tta cct			243
Lys Gly Lys Gly Ala Ile Gly Lys Arg Gly Lys Met Gly Leu Pro			
60	65	70	
gga gcc acc gga aat cca ggg gaa aag gga gaa aag gga gat gct ggt			291
Gly Ala Thr Gly Asn Pro Gly Glu Lys Gly Glu Lys Gly Asp Ala Gly			
75	80	85	
gaa ctg ggt cta cct gga aat gag ggc cca cca ggg cag aaa ggt gac			339
Glu Leu Gly Leu Pro Gly Asn Glu Gly Pro Pro Gly Gln Lys Gly Asp			
90	95	100	105
aag gga gac aaa gga gac gtg tcc aat gac gtg ctt ttg aca ggt gcc			387
Lys Gly Asp Lys Gly Asp Val Ser Asn Asp Val Leu Leu Thr Gly Ala			
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Lys Gly Asp Gln Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly Pro Pro			
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Gly Pro Pro Gly Ser Arg Arg Ser Lys Gly Pro Arg Pro Pro Asn Val			
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Phe Asn Ser Gln Cys Pro Gly Glu Thr Cys Val Ile Pro Asn Asp Asp			
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acc ttg gtg gga aga gct gat gag aaa gca aat gaa cgc cat tca cca			579
Thr Leu Val Gly Arg Ala Asp Glu Lys Ala Asn Glu Arg His Ser Pro			
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caa aca gaa tct atg atc act tcc att ggc aac cca gcc caa gtc cta			627
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Ser Asp Asp Arg Ile Trp Val Thr Glu His Phe Ser Gly Ile Met Val			
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aag gag ttc aaa gac ctg ccg gcg ctc ctc aat agc agc ttc acc ctc			771
Lys Glu Phe Lys Asp Leu Pro Ala Leu Leu Asn Ser Ser Phe Thr Leu			
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Leu His Leu Pro His Tyr Phe His Gly Cys Gly His Ala Val Tyr Asn			
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aac tct ctc tac tac cac aaa gga ggc tcc aac acc ata gtg aga ttt			867
Asn Ser Leu Tyr Tyr His Lys Gly Gly Ser Asn Thr Ile Val Arg Phe			
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tat ttt gat cga aaa tac ctc ttt gca aat tcc aag act tac ttc aac Tyr Phe Asp Arg Lys Tyr Leu Phe Ala Asn Ser Lys Thr Tyr Phe Asn 300 305 310	963
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35 40 45
Asp Gly Gln Pro Gly Leu Gln Gly Pro Lys Gly Glu Lys Gly Ala Ile
50 55 60
Gly Lys Arg Gly Lys Met Gly Leu Pro Gly Ala Thr Gly Asn Pro Gly
65 70 75 80
Glu Lys Gly Glu Lys Gly Asp Ala Gly Glu Leu Gly Leu Pro Gly Asn
85 90 95
Glu Gly Pro Pro Gly Gln Lys Gly Asp Lys Gly Asp Lys Gly Asp Val
100 105 110

Ser Asn Asp Val Leu Leu Thr Gly Ala Lys Gly Asp Gln Gly Pro Pro
115 120 125

Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly Ser Arg Arg
130 135 140

Ser Lys Gly Pro Arg Pro Pro Asn Val Phe Asn Ser Gln Cys Pro Gly
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Glu Thr Cys Val Ile Pro Asn Asp Asp Thr Leu Val Gly Arg Ala Asp
165 170 175

Glu Lys Ala Asn Glu Arg His Ser Pro Gln Thr Glu Ser Met Ile Thr
180 185 190

Ser Ile Gly Asn Pro Ala Gln Val Leu Lys Val Arg Glu Thr Phe Gly
195 200 205

Thr Trp Met Arg Glu Ser Ala Asn Lys Ser Asp Asp Arg Ile Trp Val
210 215 220

Thr Glu His Phe Ser Gly Ile Met Val Lys Glu Phe Lys Asp Leu Pro
225 230 235 240

Ala Leu Leu Asn Ser Ser Phe Thr Leu Leu His Leu Pro His Tyr Phe
245 250 255

His Gly Cys Gly His Ala Val Tyr Asn Asn Ser Leu Tyr Tyr His Lys
260 265 270

Gly Gly Ser Asn Thr Ile Val Arg Phe Glu Phe Gly Lys Glu Thr Pro
275 280 285

Gln Thr Leu Lys Leu Glu Asn Ala Leu Tyr Phe Asp Arg Lys Tyr Leu
290 295 300

Phe Ala Asn Ser Lys Thr Tyr Phe Asn Ile Ala Val Asp Glu Lys Gly
305 310 315 320

Ile Trp Ile Ile Tyr Ala Ser Ser Val Asp Gly Ser Ser Ile Leu Val
325 330 335

Ala Gln Leu Asp Gly Arg Thr Phe Ser Val Thr Gln His Ile Asn Thr
340 345 350

Thr Tyr Pro Lys Ser Lys Ala Gly Asn Ala Phe Ile Ala Arg Gly Ile
355 360 365

Leu Tyr Val Thr Asp Thr Lys Asp Thr Arg Val Thr Phe Ala Phe Asp
370 375 380

Leu Leu Gly Gly Lys Gln Ile Asn Ala Asn Phe Asp Phe Arg Met Ser
385 390 395 400

Gln Ser Val Leu Ala Met Leu Ser Tyr Asn Met Arg Asp Gln His Leu
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Asp Leu Cys Asn Ser Thr Lys Gly Ile Cys Leu Thr Gly Pro Pro Gly		
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Ala Gly Gly Leu Pro Gly His Asn Gly Leu Asp Gly Gln Pro Gly Pro
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Gln Gly Pro Lys Gly Glu Lys Gly Ala Asn Gly Lys Arg Gly Lys Met
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ggg ata cct gga gct gca gga aat cca ggg gaa agg gga gaa aag gga 240
 Gly Ile Pro Gly Ala Ala Gly Asn Pro Gly Glu Arg Gly Glu Lys Gly
 65 70 75 80

gac cat ggt gaa ctg ggc ctg cag gga aat gag ggc cca cca ggg cag 288
 Asp His Gly Glu Leu Gly Leu Gln Gly Asn Glu Gly Pro Pro Gly Gln
 85 90 95

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Lys Gly Glu Lys Gly Asp Lys Gly Asp Val Ser Asn Asp Val Leu Leu
          100          105          110

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Gly Ala Lys Gly Asp Gln Gly Pro Pro Gly Pro Pro Gly
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Pro Pro Gly Pro Pro Gly Pro Pro Gly Ser Arg Arg Ala Lys Gly Pro
130 135 140

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Arg Gln Pro Ser Met Phe Asn Gly Gln Cys Pro Gly Glu Thr Cys Ala
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tga 1203

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35 40 45

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50 55 60

Gly Ile Pro Gly Ala Ala Gly Asn Pro Gly Glu Arg Gly Glu Lys Gly
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Asp His Gly Glu Leu Gly Leu Gln Gly Asn Glu Gly Pro Pro Gly Gln
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Lys Gly Glu Lys Gly Asp Lys Gly Asp Val Ser Asn Asp Val Leu Leu
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Pro Pro Gly Pro Pro Gly Pro Pro Gly Ser Arg Arg Ala Lys Gly Pro
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Ile Pro Asn Asp Asp Thr Leu Val Gly Lys Ala Asp Glu Lys Ala Lys
165 170 175

Ser Met Ile Thr Ser Ile Gly Asn Pro Val Gln Val Leu Lys Val Thr
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Glu Thr Phe Gly Thr Trp Ile Arg Glu Ser Ala Asn Lys Ser Asp Asp
195 200 205

Arg Ile Trp Val Thr Glu His Phe Ser Gly Pro Pro Ser Ile Leu Phe
210 215 220

Pro Trp Leu Trp Ala Arg Cys Leu Gln Gln Leu Ser Leu Leu Pro Gln
225 230 235 240

Arg Gly Phe Glu Phe Gly Gln Glu Thr Ser Gln Thr Leu Lys Leu Glu
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Asn Ala Leu Tyr Phe Asp Arg Lys Tyr Leu Phe Ala Asn Ser Lys Thr
260 265 270

Tyr Phe Asn Leu Ala Val Asp Glu Lys Gly Leu Trp Ile Ile Tyr Ala
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Ser Ser Val Asp Gly Ser Ser Ile Leu Val Ala Gln Leu Asp Glu Arg
290 295 300

Thr Phe Ser Val Val Gln His Val Asn Thr Thr Tyr Pro Lys Ser Lys
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325 330 335

Lys Asp Met Arg Val Thr Phe Ala Phe Asp Leu Leu Gly Gly Lys Gln
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355 360 365

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His Leu Met Leu Tyr Pro Val Gln Phe Leu Ser Thr Thr Leu Asn Gln
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<210> 6
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